



CGCTCAGGATATGACTTCGCTAGGATCGGATCCCCGGGCTATTATATAGCTCGATCGATCT
 TTCTCTATATCCCGGATATGGGATATATACACACACACCGCGGATAGCATGACTGATCTA
 CCCCACCTTCCTTCGTCATGCTTCCTTCGTCATGCTTCCTTCGTCATGCTTCCTTCGTCAT
 CACAGACTACCGCTTCCTTCGTCATGCTTCCTTCGTCATGCTTCCTTCGTCATGCTTCCTTCG

Entrez

PubMed

Nucleotide

Protein

Genome

Structure

PMC

Taxonomy

Boo

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☐ 1: X96983. Reports B.subtilis chromo...[gi:1239975]

Links

LOCUS BS75DGREG 21808 bp DNA linear BCT 05-JUL-1999
 DEFINITION B.subtilis chromosomal DNA (region 75 degrees: cspB upstream of
 glpPFDK operon).

ACCESSION X96983

VERSION X96983.1 GI:1239975

KEYWORDS cold shock protein; cspB gene; yhcA gene; yhcB gene; yhcC gene;
 yhcD gene; yhcE gene; yhcF gene; yhcG gene; yhcH gene; yhcI gene;
 yhcJ gene; yhcK gene; yhcL gene; yhcM gene; yhcN gene; yhcO gene;
 yhcP gene; yhcQ gene; yhcR gene; yhcS gene; yhcT gene; yhcU gene;
 yhcV gene; yhcW gene; yhcX gene; yhcY gene.

SOURCE Bacillus subtilis

ORGANISM Bacillus subtilis

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

REFERENCE 1 (bases 4956 to 5615)

AUTHORS Willmsky,G., Bang,H., Fischer,G. and Marahiel,M.A.

TITLE Characterization of cspB, a Bacillus subtilis inducible cold shock
 gene affecting cell viability at low temperatures

JOURNAL J. Bacteriol. 174 (20), 6326-6335 (1992)

MEDLINE 93015680

PUBMED 1400185

REFERENCE 2

AUTHORS Beijer,L., Nilsson,R.P., Holmberg,C. and Rutberg,L.

TITLE The glpP and glpF genes of the glycerol regulon in Bacillus
 subtilis

JOURNAL J. Gen. Microbiol. 139 (Pt 2), 349-359 (1993)

MEDLINE 93171878

PUBMED 8436953

REFERENCE 3 (bases 1 to 21808)

AUTHORS Noback,M.A., Terpstra,P., Holsappel,S., Venema,G. and Bron,S.

TITLE A 22 kb DNA sequence in the cspB-glpPFDK region at 75 degrees on
 the Bacillus subtilis chromosome

JOURNAL Microbiology (Reading, Engl.) 142 (Pt 11), 3021-3026 (1996)

MEDLINE 97124185

PUBMED 8969498

REFERENCE 4 (bases 1 to 21808)

AUTHORS Noback,A.

TITLE Direct Submission

JOURNAL Submitted (22-MAR-1996) Noback M. A., University of Groningen,
 Dept. of Genetics, Kerklaan 30, Haren, 9751 NN The Netherlands

FEATURES Location/Qualifiers

source

1..21808

/organism="Bacillus subtilis"

/mol_type="genomic DNA"

/strain="168"

/db_xref="taxon:1423"

/map="75 degrees, upstream of glpPFDK"

gene

1..256

/gene="yhcA"

CDS

<1..256

BEST AVAILABLE COPY

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/db_xref="GI:1239976"
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/db_xref="UniProt/Swiss-Prot:P54585"
/translation="SNLMVMNMVSYDTAKTYVYSHIYKHASLDSNVMGINDAFMWATL
FCVAGLILSIFLRDVRKDKLRKKKKEELSLLPAPKEAKES"
gene join(264..270,279..809)
RBS /gene="yhCB"
264..270
/gene="yhCB"
CDS 279..809
/gene="yhCB"
/note="similarity to trp repressor-binding protein wrbA
from Escherichia coli (Swiss Prot P304849) and to
flavodoxin from Clostridium acetobutylicum (Swiss Prot
P18855)."
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gene join(808..816,822..1196)
RBS /gene="yhCC"
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/gene="yhCC"
CDS 822..1196
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ESDKMQDRSYRDALLSMKNKKK"
gene 1186..1190
/gene="yhCD"
RBS 1186..1190
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gene 1196..1351
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CDS 1196..1351
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PRIFSGR"
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gene 1343..1348
/gene="yhce"
RBS 1343..1348
/gene="yhce"
gene 1356..2117
/gene="yhce"
CDS 1356..2117
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SLRNWRGMRWAAMVLLVAMWLFDEYIIISPLVESQKHFWPVTVYCNFDFHFNWVRLE
LKPIHLSVLGFPIAIVITFLLLIMASKLLDRKVEV"
gene 2108..2112
/gene="yhcf"
RBS 2108..2112
/gene="yhcf"
gene 2120..2485
/gene="yhcf"
CDS 2120..2485
/gene="yhcf"
/note="similarity to members of the gntR regulator family
like the korA protein from Streptomyces lividans (Swiss
Prot P22405) and farR from Escherichia coli (Swiss Prot
P13669)."
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LGLTKEEMLEGIKTFTEGG"
gene 2473..2481
/gene="yhcg"
RBS 2473..2481
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gene 2487..3185
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CDS 2487..3185
/gene="yhcg"
/note="similarity to ABC transporters like the sulfate
transport protein cysA from Synechococcus (Swiss Prot
P14788) and the copper transport protein nosF from
Pseudomonas stutzeri (Swiss Prot P19844)."
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/db_xref="UniProt/Swiss-Prot:P54591"
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FHTEQVYKLLNEMQLNPEKKIKKLSKGNRGLKIVLALARRADVILLDEPFSGLDPMV
RDSIVNSLVSYIDFEQQIVVIATHEIDEIETLLDEVIILANGEKVAQREVEDIREQEG
MSVLQWFKSKMEVC"
gene join(3187..3195,3202..4119)
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RBS 3187..3195
/gene="yhch"
CDS 3202..4119
/gene="yhch"
/note="similarity to ABC transporters like the copper
transport protein nosF from Pseudomonas stutzeri (Swiss
Prot P19844) and yhcG (this submission)."
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/db_xref="UniProt/Swiss-Prot:P54592"
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RMVKGVTKEKIDEVVELVGLTDRIHDKVKTYSLGMRQRLGLAQCLLDHPKVLILDEPT
NGLDPAGIREIRDHLKKLTRERGMVIVSSHLLSEMELMCDRIAILQKGLIDIQNVK
DENIDENDTYFFQVEQPSEAATVLNQYDLLSKTNGVEIKLAKEEVPVAVIELLMQQIR
IYEVKVITKSLEDRFLEMTGETKEEVQHA"
gene 4097..4105
/gene="yhci"
RBS 4097..4105
/gene="yhci"
gene 4112..5053
/gene="yhci"
CDS 4112..5053
/gene="yhci"
/note="similarity to the membrane protein nosY from
Pseudomonas stutzeri, involved in copper processing (Swiss
Prot P19845)."
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NSHWKQELQAQNAELKKEIKEDPSLKDGYKETITLNDYRIEHNIPSDTGYTVWSYVTD
SANFTILTGLFTIIIAAGIVANEFNWGTIKLLMIRPLSRFQILMSKYITVLLFGLLLL
LILFIGSTLLGLIFFGTGGETAANIHLIYKDGHVIEQNMMGHLATTYLSSESVSALMVA
TMAFMLSAVFRNSSLAVGFSIFLLVAGTTATAFIAAKFDWAKYILFANVDLTQYVDGT
PLIKGMTMTFSLVMLAIYFIIFLLLAFGIFMKRDIAN"
conflict 4969..4970
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conflict /replace="t"
4973
/gene="yhcI"
/citation=[1]
/replace="g"
conflict 4990
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terminator 5055..5091
terminator complement (5100..5129)
conflict 5143..5144
/citation=[1]
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gene complement (5145..5361)
/gene="cspB"
CDS complement (5145..5348)
/gene="cspB"
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RBS complement (5356..5361)
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conflict 5478
/citation=[1]
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conflict 5523
/citation=[1]
/replace="cc"

gene 5769..6575
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RBS 5769..5773
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CDS 5784..6575
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Escherichia coli (Swiss Prot P04846)."
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PLGT
TYITPMGIYSKRYERIRDISRGAVVSVDPKAFDFGRALTVLQEAGLLTLKNGFNGTGS
VDMIKDNPRHLKLKAVRQQDAVSGADVFMKPSEAKKAGLNPKKHTLKSGGLMSEEM
NLIVVRAEDQDREALQTILELYQADDTAAFIEKEYQGDLVRLFCL"
terminator 6593..6624
gene complement (6616..7709)
/gene="yhck"

CDS

complement(6616..7695)
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Streptomyces ambofaciens (Swiss Prot P36892) and ORF3 from
Vibrio anguillarum (Genbank U17054)."
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GLLGVLVMVFGFTYQHSIIDLRNIPIMIAALYGGWVSTATALAMITAGRLLITMNTSA
LYSVIIICIAAIPSLIVSRKKVQLKHAFYLLIITNSLISFSFYFLIDLHSYELHLYF
WIISIAGGMSLYIIDHETNAHLLFKQYKQAHFDFLTGVYNRRKFEETTKALYQQA
DTPHFQFALIYMDIDHFKTINDQYGHHEGDQVLKELGLRLKQTIRNTDPAARIGGEF
AVLLPNCSLDKAARIAERIRSTVSDAPIVLTNGDELSVTISLGAAYHPNNTTEQPGSLP
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RBS

complement(7705..7709)

gene

/gene="yhck"

7849..9259

RBS

/gene="yhcl"

7849..7857

CDS

/gene="yhcl"

7868..9259

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protein gltT from Bacillus caldotenax (Swiss Prot
P24944)."
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VDAVYAIVMRVVTLILRLTPYGVLAIMTKTIATSDLSILKLGMFVIAASYAALITMFI
IHLLLLTFSGLPVPIYLKAVPVLVFAFTSRSSAGALPLNIKTQSRSMGVPEGIANFAG
SFGLSIGQNGCAGIYPAMLAMMIAPTGVGNPFDPVFIITVIAVVAISSFGVAGVGGGA
TFAALLVLSSLNMPVALAGLLISIEPLIDMGRTALNVSGSMTSGLITSKVTKEIDQGA
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terminator

9266..9297

gene

complement(9299..9765)

/gene="yhcm"

CDS

complement(9299..9754)

/gene="yhcm"

/note="glutamine-rich protein."
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/db_xref="UniProt/Swiss-Prot:P54597"
/translation="MLFNQRRGISPAALIIGSTMLITALSPQIRQIRISGFITGMNRR
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TQSQTRQTETAAKKRQPHYAEPIHFEQNAMNVMDNTMMEMLEDLEPGR"
RBS complement (9757..9765)
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gene 9890..10473
/gene="yhcN"
RBS 9890..9897
/gene="yhcN"
CDS 9904..10473
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/note="asparagine-rich protein. Similarity to CS3 pili
synthesis protein from Escherichia coli (Swiss Prot
P15487)."
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GKRIQNGDPIAGLFEFTQTQTVQRFVFNAE"
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gene join(10641..10644,10653..10952)
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gene 10943..11560
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KDFKKKFEKNSAALDSIYPMPLLLVKSLLTHSALCRRHLSLGRGE"
gene complement(join(11492..12145,12153..12160))
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CDS complement(11492..12145)
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Bacillus subtilis (Swiss Prot P23261)."

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complement(12153..12160)
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join(12217..12222,12228..15881)
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12217..12222
/gene="yhcR"
12228..15881
/gene="yhcR"
/note="similarity (C-terminal half) to UDP-sugar hydrolase
precursor (ushA) from Escherichia coli (Swiss Prot
P07024)."
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INGSLGDQYEGRLVKLTAFVSSIPSSPAGGGYNVTMIDDDHAMTLRVMNETGVINEL
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KDQKGIWNENDPLMEMPFREFRAREQGKGLTRYVGDSSNKTYVQPADWKKIAVENRIF
ASASEAESAGYKKRQTAPQEHVPLRILSMNDLHGKIDQQYELDLGNGTVDGTGFRMD
YAAAYLKEKKAEEKNSLIVHAGDMIGGSSPVSSLLQDEPTVELMEDIGFDVGTGNGHE
FDEGTDELLRILNGGDHPKGTSGYDQGNFPLVCANCKMKSTGEPFLPAYDIINVEGVP
VAFIGVVTQSAAGMVMPEGIKNIEFTDEATAVNKAEEELKKKGVKAIIVLAHMSAEQN
GNAITGESADLANKTDEIDVIFAHNHQVVNGEVNGKLIVQAFEYGAIGVVDVEID
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SIITLQHEKEELILTTCYPFSYVGNAPKRYIIYGKRV T"
16473..16501
terminator
gene complement(16504..17427)
/gene="yh cT"
CDS complement(16504..17412)
/gene="yh cT"
/note="Similarity to DRAP deaminase from Saccharomyces
cerevisiae (PIR S50972) and to a family of hypothetical
proteins like yceC from Escherichia coli (Swiss Prot
P23851)."
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/db_xref="UniProt/Swiss-Prot:P54604"
/translation="MNQKGRGLEILINEKQDGQWLFSLKTKALKASKPVIQDWMSHQQ
IKVNHESVLNNMIVKKGDRVFIDLQSEASSVIPEYGELDILFEDNHMLIINKPAGIA
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/note="This is the N-terminal fragment of a hypothetical protein from which the C-terminal sequence has been published (ORF1 in [3] and YHXA_BACSU in Swiss Prot : P33189). Unpublished sequence from the authors in [3] contains the complete sequence of yhxA. Similarity to DAPA aminotransferase (bioA) from Bacillus sphaericus (Swiss Prot P22805)."

/citation=[2]

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